



M L A G G Y R 7
 GAGGCCAGCTGTTTCCACCCATTCACCCAGGG ATG CTG GCG GGG GGC GTG AGG 151
 S M P S P L L A C W Q P I L L L V L G S 27
 AGC ATG CCC AGC CCC CTC CTC CCT TCC TCC CAG CCC ATC CTC CCT CCT CCT GTG CTC CCC TCA 211
 V L S G S A T G C P P R C E C S A Q D R 47
 GTG CTG TCA GGC TCC GGC AGG GGC TCC CCT CCT CCT TCC GAG TCC TCC GGC CCT GAG CCT 271
 A V L C H R K R F V A V P E G I P T E T 67
 CCT CTG CCT TCC CAC CCC AAG CCG TTT GTG GCA GTC CCT GAG GGC ATC CCC ACC GAG ACC 331
 R I L D L G K N R I K T L N Q D E F A S 87
 CCC CCTG GAC CTC GGC AAG AAC CCC ATC AAA ACC CTC AAC CAG GAC GAG TTC GGC AGC 391
 F P H L E E L E L N E N I V S A V E P G 107
 TCC CCTG GAG GAG CCTG GAG CCT AAC GAG AAC ATC GTG AGC GGC CCTG GAG CCC GGC 451
 A F N N L F N L R T L G L R S N R L K I 127
 CCT TTC AAC AAC CTC TTC AAC CTC CCT ACC CCT GGT CCT CCT CCT AAC AAC CCC CCTG AAG CCT 511
 I P L G V F T G L S N L T K L D T R E N 147
 ATC CCTG CTC GGC GTC TTC ACT GGC CCT AAC AAC CCTG ACC AAC AAC CCTG GAC AGC AGG GAG AAC 571
 K I V I L L D Y M F Q D L Y N L K S L E 167
 AAC ATC CCTG CTC GAC TAC ATG TTT CAG GAC CCTG TAC AAC CCTG AAC TCA CCTG GAG 631
 V G D N D L V Y I S H R A F S G L N S L 187
 CCT CCTG AAC GAC CTC GTC TAC ATC CCT CCT AAC CCTG AAC CCTG AAC CCTG AAC CCTG 591
 E Q L T L E K C N L T S I P T E A L S H 207
 AAC CCTG ACT CCTG GAG AAA TCC AAC CCTG ACC CCT CCT AAC ATC AAC CCTG AAC CCTG CCT CCT 651
 C H G L I V L R L R H L N I N A I R D Y 227
 CCTG CCTG AAC CCTG CCTG AAC CCTG CCT CCT AAC CCT CCT AAC CCTG AAC CCTG CCT CCT 611
 S F K R L Y R L K V L E I S H W P Y L D 247
 CCTG CCTG AAC CCTG CCTG AAC CCTG CCT CCT AAC CCT CCT AAC CCTG CCT CCT 671
 T M T P N C L Y G L N L T S L S I T H C 267
 AAC ATG AAC CCC AAC CCT CCT TAC CCT CCT AAC CCT CCT AAC CCT CCT AAC CCT CCT 731
 N L T A V P Y L A V R H L V Y L R F L N 287
 AAC CCTG CCT 791
 L S Y N P I S T I E G S M L H E L L R L 307
 CCT 851
 Q E I Q L V G G Q L A V V E P Y A F R G 327
 AAC CCT 911
 L N Y L R V L N V S G N Q L T T L E E S 347
 CCT 971

FIG. 1A

FIG. 1B

FIG. 2

Percent Similarity: 49.308 Percent Identity: 29.412

T79 1 MLAGGVRSMPSPLLACWQPILLVLGSVLSGS..ATGCPPRCECSAQDR. 47
D45913 1MARLSTGKAAC.QVVLGLLITSLTESSILTSEC2QLCVCEIRPWF 44

T79 48AVLCHRKRKVAVPEGIPTETRLLDLGKNRIKTLNQDEFAS 87
D45913 45 TPQSTYREATTVDCNDLRLTRIPGNLSSDTQVLLLQSNNI..... 84

T79 88 FPHLEELNENIVSAVEPGAFNNLFNLRTLGLRSNRLKLIPLGVFTGLS 137
D45913 85AKTVDELQQLFNLTEDFSQNNFTNIKEVGLANLT 119

T79 138 NLTKLDTRENKIVILLDYMFQDLYNLKSLEVGNDLVYISHRAFSGLNSL 187
D45913 120 QLTTLHLEENQISEMTDYCLQDLSNLQELYINHNQISTISANAFSGLKNL 169

T79 188 EQLTLEKCNLTSIPTEALSHLHGLIVLRLRHILNINAIRDYSFKRLYRLKV 237
D45913 170 LRLHILNSNKLKVIDSRWFDPNLEILMIGENPVGILDMMNFRPLSNLRS 219

T79 238 LEISHWPYLDTMTPNCLYGLN.LTSLSITHCNLTAVPYLAVRHLVYLRFL 286
D45913 220 LVLAG.MYLTDVDGNALVGLDSLESLSFYDNKLIKVPOLALQKVPNLKFL 268

T79 287 NLSYNPISTIEGSMHELLRLQEIQLVG.GQLAVVEPY..... 323
D45913 269 DLNKNPIHKIQEGDFKNMLRLKELGINNMGELVSDRYALDNLPELTKE 318

T79 324AFRGLNYLRVLNVSGNQLTLEESVFHSVGNLLETLIL 360
D45913 319 ATNNPKLSYIHRLAFRSVPALESMLNNNALNAVYQKTVESLPNLREISI 368

T79 361 DSNPLACDCRLLWVFRRRWRLNFRQQPT.CATPEFVQGKEFKDFPDVLL 409
D45913 369 HSNPLRCDCVIHWINSNKTNIRFMEPLSMFCAMPPEYRGQQVK...EVLI 415

T79 410 PNYFT.CRRARIIDRKAQQVFVDEGHTVQFVCRADGDPPIALWLSPRKH 458
D45913 416 QDSSEQCLPMISHDTFPNHLNMDIGTTLFLDCRAMAEPEPEIYWVTPIGN 465

T79 459 LVSAKS.NGRLTVFPDGTLLEVRYAQVQDNGTYLCIAANAGGNDMPAHLH 507
D45913 466 KITVETLSDKYKLSSEGTLIEIANIQIEDSGRYTCVAQNVQGADTRVATIK 515

T79 508 V.....RSYSPDWPHQ 518
D45913 516 VNGTLLDGAQVLKIVVKQTESHSILVSWKVNSNVMTSNLKWSATMKIDN 565

T79 519 PNKTF.....AFISNQPGEGEANSTRA 540

FIG. 3A

|: |: . | . | . . | |
D45913 566 PHITYTARVPVDVHEYNLTHLQPSTDYEVCLTVSNIHQQTQKSCVNVTTK 615
|..|:|:||.. . .|.: : |:::|: . . : ::: .| | .. |:
T79 541 TYPFPFDIKTLIATTMGFI..SFLGVVLFCVLVLLFLWSRGKGNTKHNIE 588
D45913 616 TAAFALDISDHETSTALAAVMGSMFAVISLASIAIYIAKRFKRKNYHSL 665
|..|:|:||.. . .|.: : |:::|: . . : ::: .| | .. |:
T79 589 IEYVPRKSDAGISSADAPRKFNMKMI..... 614
D45913 666 KKYMQKTSSIPNLNELL.YPPLINLWEADSDKDKDGSADTKPTQVDTSRSYY 714

FIG. 3B

09803589-031502

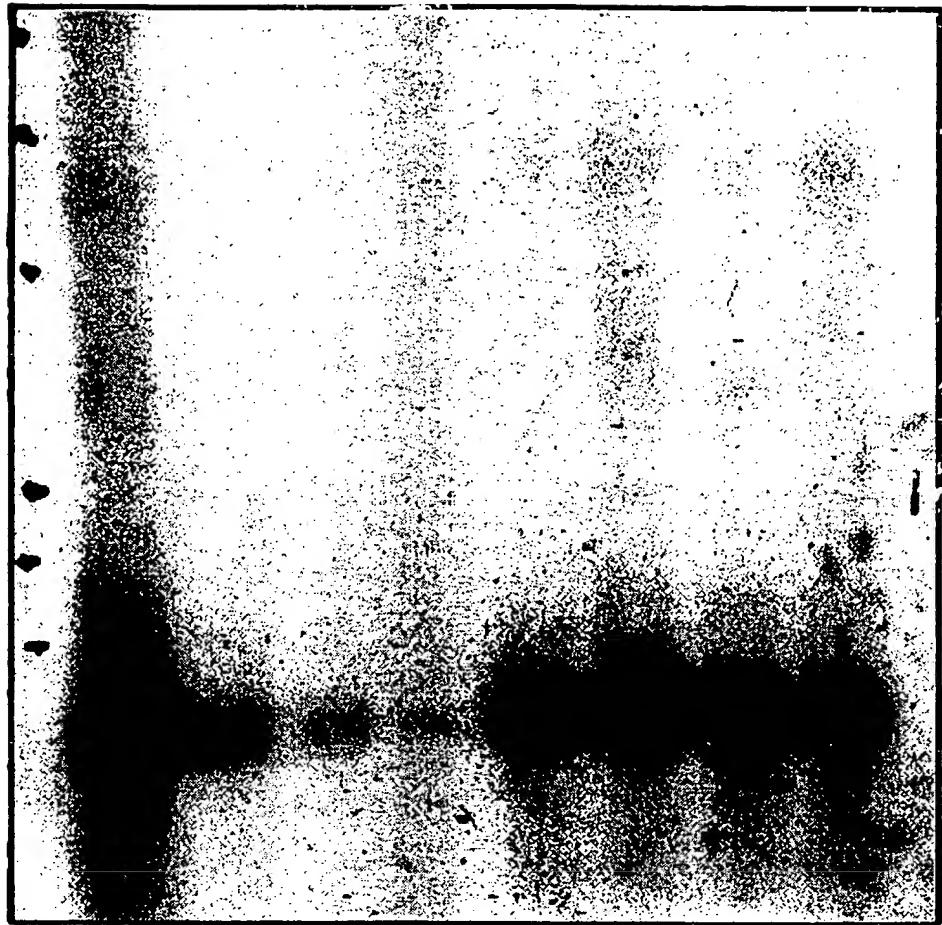


FIG. 4

09803589 - 011502

T R P I L V I H D E S Q K G P E V T S N 19
 CC ACG CGT CCS ATC TTC GTC ATC CAC GAT GAA CAG AAG CGG CCT GAA GTG ACC TCC ATC 59
 59
 A A L T L R N F C N W Q K Q H N P P S D 19
 CCT CCT CTC ACT CCT CGG AAC TTT TCC AAC TCG CAG AAG CAG CAC AAC CCT CGG AGT GAC 119
 119
 R D A E H Y D T A I L F T R Q D L C G S 59
 CGG GAT GCA GAG CAC TAT GAC ACA GCA ATT CCT TTC ACC AGA CAG GAC TTC TGT CGG TCC 179
 179
 Q T C D T L G M A D V G T V C D P S R S 79
 CGG ACA TGT GAT ACT CCT CGG ATG GCT GAT GTT GCA ACT GTG TGT GAT CGG AGC AGA AGC 239
 239
 C S V I E D D G L Q A A F T T A H E L G 99
 TGC TCC GTC ATA GAA GAT GAT GGT TTA CAA GCT GCC TTC ACC ACA CCT CAT GAA TTA CGC 299
 299
 H V F N M P H D D A K Q C A S L N G V N 119
 CGC GTG TTT AAC ATG CCA CAT GAT GAT GCA AAG CGG TGT GCC AGC CTT AAT GGT GTG AAC 359
 359
 Q D S H M M A S M L S N L D H S Q P W S 119
 CGG GAT TCC CTC ATG ATG CGG TCA ATG CCT TCC AAC CCT GAC CAC AGC CGG CCT TGG TCT 419
 419
 P C S A Y M I T S F L D N G H G E C L M 159
 CCT TCC AGT GCG TAC ATG ATT ACA TCA TTT CTG GAT AAT GGT CAT CGG GAA TGT TGG ATG 479
 479
 D K P Q N P I Q L P G D L P G T S Y D A 179
 GAC AAG CCT CGG AAC ATA CGG CCT CCA GAT CCT CCT CGC ACC TCG TAC GAT CCT 539
 539
 N R Q C Q F T F G E D S K H C P D A A S 199
 AAC CGG CGG TCC CGG TTT ACA TTT CGG GAG GAC TCC AAA CAC TCC CCT GAT GCA GCC AGC 599
 599
 T C S T L W C T G T S G G V L V C Q T K 219
 ACA TGT AGC ACC TTG TGG TGT ACC CGC ACC TCT GGT CGG GTG CTG GTG TGT CAA ACC AAA 659
 659
 H F P W A D G T S C G E G K W C I N G K 239
 CGC TCC CGG TGG GCG GAT CGC ACC AGC TGT GGA GAA CGG AAA TGG TGT ATC AAC CGC AAG 719
 719
 C V N K T D R K H F D T P F H G S W G M 259
 TGT GTG AAC AAA ACC GAC AGA AAG CAT TTT GAT ACG CCT TTT CAT GGA AGC TGG GGA ATG 779
 779
 W G P W G D C S R T C G G G V Q Y T M R 279
 TGG CGG CCT TGG CGG GAC TGT TCG AGA AGC TCC CCT CGG GGA GTC CAG TAC ACG ATG ACG 839
 839
 E C D N P V P K N G G K Y C E G K R V R 299
 GAA TGT GAC AAC CCT GTC CCT AAG AAT CGA CGG AAG TAC TGT GAA GGC AAA CCT GTG CGC 999
 999
 Y R S C N L E D C P D N N G K T F R E E 319
 TAC AGA TCC TGT AAC CCT GAG GAC TGT CCT GAC AAT AAT CGA AAA ACC TTT AGA GAG GAA 959
 959
 Q C E A H N E F S K A S F G S G P A V E 339
 CAA TGT GAA CGA CAC AAC CGG TTT TCA AAA GCT CCT TTT CGG AGT CGG CCT CGG GTG GAA 1019
 1019
 W I P K Y A G V S P K D R C K L I C Q A 359
 TGG ATT CCT CGG AAC CCT CGC GTC TCA CCT AAG GAC AGG TCC AAG CTC ATC TCC CAA CGC 1079
 1079
 K G I G Y F F V L Q P K V V D G T P C S 379
 AAA CGG ATT CGC TAC TTC TTC GTT TGG CAG CCT AAG GTT GTA GAT GGT ACT CCT TGT AGC 1139
 1139

FIG. 5B

FIG. 5C

卷之三

0930035899 - 09414502

251 DQSMADFHGSGLKHVLLTLEVAARFYKHPHSIRNSISLWVVKILVYEQ 300
 ||||.::||
 1TROPILVIRHEDQ 11

 301 KGPEVTSNAAALTLLRNFCSWQRQHNSPSDROPEHYDTAILFTRQDLCGSHT 350
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:
 12 KGPEVTSNAAALTLLRNFCSWQRQHNSPSDRODAEYDITAILFTRQDLCGSQT 61

 351 CDTLGNAADVTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDACK 400
 |||||:|||||:
 62 CDTLGNAADVTVCDPSRSCSVIEDDGLQAAFTTAHELGHVFNMPHDACK 111

 401 CASLNGVSGDSHLMASMLSSLHSQPNSPCSAIVMTSFLDNGHGECLMOK 450
 |||||..:|||||:
 112 CASLNGVNQOSHMMASMLSNLHSQPNSPCSAIVMTSFLDNGHGECLMOK 161

 451 PQNPIKLPSDLPGTLYDANRQCQFTTGEESKHCPOAASTCTTWCIGTSG 500
 ||||.||:|||||:
 162 PQNPIQLPGDLPGTSYDANRQCQFTTGEDESKHCPOAASTCSTWCIGTSG 211

 501 GLLVCQTTKHFPAWADGTSCEGKWCVSGKCVNKTOMKHFATPVHGSNGPAG 550
 ||:|||||:
 212 GVLVCQTTKHFPAWADGTSCEGKWCINGKCVNKTOMKHFATPVHGSNGPAG 261

 551 PWGDCSRTOGGVQYTMRCDINPVPRNGKCYCEGKRVYRSCNIEDCPDN 600
 |||||:
 262 PWGDCSRTOGGVQYTMRCDINPVPRNGKCYCEGKRVYRSCNIEDCPDN 311

 601 NGKTFREEQCEAHNEFSKASFGNEPTVENTPKYAGVSPKDRCKLTCENG 650
 |||||:
 312 NGKTFREEQCEAHNEFSKASFGSGPAVENIPKYAGVSPKDRCKLICQAG 361

 651 IGYFFVLQPKVVDGTPCSPDSTSVCVQQQCVKAGCDRIIDSKKCFDAGV 700
 |||||:
 362 IGYFFVLQPKVVDGTPCSPDSTSVCVQQQCVKAGCDRIIDSKKCFDAGV 411

 701 CGGNGSTCKKMSGIVTSTRPGYHDIVTIPAGATNIEVKHRNQRGSRNGS 750
 |||||:
 412 CGGNGSTCKKLSGSVTSKPGYHDITIPTGATNIEVKQRNQRGSRNGS 461

 751 FLAIKAADGTYILNGNFTLSTLEQDLYKGTVLYSGSSAALERIRSFSP 800
 |||||:
 462 FLAIKAADGTYILNGNFTLSTLEQDLYKGVVLYSGSSAALERIRSFSP 511

 801 LKEPLTIQVLMVGHALRPKDGFYFMRKQTESFNAIPTPSAWVIEENGEC 850
 |||||:
 512 LKEPLTIQVLMVGHALRPKDGFYFMRKQTESFNAIPTPSAWVIEENGEC. 560

 901 WSPCSKTCGKGYKQRNLKCVSHDGGVLSNESCDPLKKPKHYIDFCILTOC 950
 |||||:
 561 ...CSKTCGKGYKQRSLKCLSHDGGVLSHESCDPLKKPKHYIDFCILTOC 607

 951 S* 951
 |
 608 S* 609

FIG. 6

0930353535 - 0930353535
 gtgcctac atg gtc acg tcc ttc cta gat aat gga cac ggg gaa tgt ttg 50
 Met Val Thr Ser Phe Leu Asp Asn Gly His Gly Glu Cys Leu
 1 5 10

atg gac aag ccc cag aat cca atc aag ctc cct tct gat ctt ccc ggt 98
 Met Asp Lys Pro Gln Asn Pro Ile Lys Leu Pro Ser Asp Leu Pro Gly
 15 20 25 30

acc ttg tac gat gcc aac cgc cag tgt cag ttt aca ttc gga gag gaa 146
 Thr Leu Tyr Asp Ala Asn Arg Gln Cys Gln Phe Thr Phe Gly Glu
 35 40 45

tcc aag cac tgc cct gat gca gcc agc aca tgt act acc ctg tgg tgc 194
 Ser Lys His Cys Pro Asp Ala Ala Ser Thr Cys Thr Thr Leu Trp Cys
 50 55 60

act ggc acc tcc ggt ggc tta ctg gtg tgc caa aca aaa cac ttc cct 242
 Thr Gly Thr Ser Gly Gly Leu Leu Val Cys Gln Thr Lys His Phe Pro
 65 70 75

tgg gca gat ggc acc agc tgt gga gaa ggg aag tgg tgt gtc agt ggc 290
 Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly Lys Trp Cys Val Ser Gly
 80 85 90

aag tgc gtg aac aag aca gac atg aag cat ttt gct act cct gtt cat 338
 Lys Cys Val Asn Lys Thr Asp Met Lys His Phe Ala Thr Pro Val His
 95 100 105 110

gga agc tgg gga cca tgg gga ccg tgg gga gac tgc tca aga acc tgt 386
 Gly Ser Trp Gly Pro Trp Gly Pro Trp Gly Asp Cys Ser Arg Thr Cys
 115 120 125

ggt ggt gga gtt caa tac aca atg aga gaa tgt gac aac cca gtc cca 434
 Gly Gly Val Gln Tyr Thr Met Arg Glu Cys Asp Asn Pro Val Pro
 130 135 140

aag aac gga ggg aag tac tgt gaa ggc aaa cga gtc cgc tac agg tcc 482
 Lys Asn Gly Gly Lys Tyr Cys Glu Gly Lys Arg Val Arg Tyr Arg Ser
 145 150 155

tgt aac atc gag gac tgt cca gac aat aac gga aaa acg ttc aga gag 530
 Cys Asn Ile Glu Asp Cys Pro Asp Asn Asn Gly Lys Thr Phe Arg Glu
 160 165 170

gag cag tgc gag gcg cac aat gag ttt tcc aaa gct tcc ttt ggg aat 578
 Glu Gln Cys Glu Ala His Asn Glu Phe Ser Lys Ala Ser Phe Gly Asn
 175 180 185 190

gag ccc act gta gag tgg aca ccc aag tac gcc ggc gtc tcg cca aag 626
 Glu Pro Thr Val Glu Trp Thr Pro Lys Tyr Ala Gly Val Ser Pro Lys
 195 200 205

FIG. 7A

09302556 - 021502

gac agg tgc aag ctc acc tgt gaa gcc aaa ggc att ggc tac ttt ttc	674		
Asp Arg Cys Lys Leu Thr Cys Glu Ala Lys Gly Ile Gly Tyr Phe Phe			
210	215	220	
gtc tta cag ccc aag gtt gta gat ggc act ccc tgt agt cca gac tct	722		
Val Leu Gln Pro Lys Val Val Asp Gly Thr Pro Cys Ser Pro Asp Ser			
225	230	235	
acc tct gtc tgt gtg caa ggg cag tgt gtg aaa gct ggc tgt gat cgc	770		
Thr Ser Val Cys Val Gln Gly Gln Cys Val Lys Ala Gly Cys Asp Arg			
240	245	250	
atc ata gac tcc aaa aag aag ttt gat aag tgt ggc gtt tgt gga gga	818		
Ile Ile Asp Ser Lys Lys Phe Asp Lys Cys Gly Val Cys Gly Gly			
255	260	265	270
aac ggt tcc aca tgc aag aag atg tca gga ata gtc act agt aca aga	866		
Asn Gly Ser Thr Cys Lys Lys Met Ser Gly Ile Val Thr Ser Thr Arg			
275	280	285	
cct ggg tat cat gac att gtc aca att cct gct gga gcc acc aac att	914		
Pro Gly Tyr His Asp Ile Val Thr Ile Pro Ala Gly Ala Thr Asn Ile			
290	295	300	
gaa gtg aaa cat cgg aat caa agg ggg tcc aga aac aat ggc agc ttt	962		
Glu Val Lys His Arg Asn Gln Arg Gly Ser Arg Asn Asn Gly Ser Phe			
305	310	315	
ctg gct att aga gcc gct gat ggt acc tat att ctg aat gga aac ttc	1010		
Leu Ala Ile Arg Ala Ala Asp Gly Thr Tyr Ile Leu Asn Gly Asn Phe			
320	325	330	
act ctg tcc aca cta gag caa gac ctc acc tac aaa ggt act gtc tta	1058		
Thr Leu Ser Thr Leu Glu Gln Asp Leu Thr Tyr Lys Gly Thr Val Leu			
335	340	345	350
agg tac agt ggt tcc tcg gct gcg ctg gaa aga atc cgc agc ttt agt	1106		
Arg Tyr Ser Gly Ser Ser Ala Ala Leu Glu Arg Ile Arg Ser Phe Ser			
355	360	365	
cca ctc aaa gaa ccc tta acc atc cag gtt ctt atg gta ggc cat gct	1154		
Pro Leu Lys Glu Pro Leu Thr Ile Gln Val Leu Met Val Gly His Ala			
370	375	380	
ctc cga ccc aaa att aaa ttc acc tac ttt atg aag aag aac gag	1202		
Leu Arg Pro Lys Ile Lys Phe Thr Tyr Phe Met Lys Lys Lys Thr Glu			
385	390	395	
tca ttc aac gcc att ccc aca ttt tct gag tgg gtg att gaa gag tgg	1250		
Ser Phe Asn Ala Ile Pro Thr Phe Ser Glu Trp Val Ile Glu Glu Trp			
400	405	410	

FIG. 7B

ggg gag tgc tcc aag aca tgc ggc tca ggt tgg cag aga aga gta gtc 1298
 Gly Glu Cys Ser Lys Thr Cys Gly Ser Gly Trp Gln Arg Arg Val Val
 415 420 425 430

 cag tgc aga gac att aac gga cac cct gct tcc gaa tgt gca aag gaa 1346
 Gln Cys Arg Asp Ile Asn Gly His Pro Ala Ser Glu Cys Ala Lys Glu
 435 440 445

 gtg aag cca gcc agt acc aga cct tgt gca gac ctt cct tgc cca cac 1394
 Val Lys Pro Ala Ser Thr Arg Pro Cys Ala Asp Leu Pro Cys Pro His
 450 455 460

 tgg cag gtg ggg gat tgg tca cca tgt tcc aaa act tgc ggg aag ggt 1442
 Trp Gln Val Gly Asp Trp Ser Pro Cys Ser Lys Thr Cys Gly Lys Gly
 465 470 475

 tac aag aag aga acc ttg aaa tgt gtg tcc cac gat ggg ggc gtg tta 1490
 Tyr Lys Lys Arg Thr Leu Lys Cys Val Ser His Asp Gly Gly Val Leu
 480 485 490

 tca aat gag agc tgt gat cct ttg aag aag cca aag cat tac att gac 1538
 Ser Asn Glu Ser Cys Asp Pro Leu Lys Lys Pro Lys His Tyr Ile Asp
 495 500 505 510

 ttt tgc aca ctg aca cag tgc agt taagaggcgt tagaggacaa gtagcgtgg 1592
 Phe Cys Thr Leu Thr Gln Cys Ser
 515

 ggaggggctg atacactgag tgcaagagta ctggaggat ccagttagtc aaaccagtaa 1652
 gcagttaggt gtggcaagga ggtgtgtta ggggatacat agcaaaggag gtagatcagg 1712
 acactaccct gccagttaca ttctgataag gtagttaatg aggcacagta gcatctgaaa 1772
 gaccatacag agcactaagg agccccaaag cactattagt atcttttc ttatatctat 1832
 cgcccaaata atttcagag tctggagaa gcccctgttc actgtactaa ctagatactt 1892
 cttatcacaa agattggaa aggcaaagca gaaagatgt aagactgggt ttcaaacaag 1952
 gcttggtttc aatcactgga ggcaaggagg aggggacaaa caagatcatt attcgaagtc 2012
 gctgggttgc gtggtttac ggaagggtga tgcatttc ctatcaacag tgaaaagttc 2072
 agcttggtca acgtgacaga aaggctcattc tccgtgaaag agctcctgat ttcttcttac 2132
 accatctcag ttcttaacta tagttcatgt tgaggtagaa acaatttcattc tatttataaa 2192
 atgtacattg gaaaaaaaaa gtgaagtttta tgaggtacac ataaaaactg aggaaacaa 2252
 tgagcaacat gcctcctgtt ttgcttcctc ctgaggtaaa cctgcctggg gattgagtt 2312
 gtttaagatt atccatggct cacaagagggc agtaaaataa tacatgttgc gccagagtt 2372
 gaatgggtta tagagatcag ggtcccatga gatggggac atgggtatca ctcatttcac 2432
 atgggaggct gctgcagggt agcagggtcca ctcctggcag ctggtccaac agtcgtatcc 2492
 tggtaatgt ctgttcagct ttctactga gagagaatat gactgttcc atatgtatat 2552
 gtatataatgta aaatatgtta ctatgaattt catgtacttt ataagtattt gttgtctgt 2612
 tccttcttaag aaggactata gtttataata aatgcctata ataacatatt tattttata 2672
 catttatttc taatgataaa acctttaagt tatatcgctt ttgtaaaagt gcatataaaa 2732
 atagagtatt tatacaatatt atgttaacta gaaataataa aagaacactt ttgaatgtgt 2792
 atgccttattt tctggagtgg gattaactt tggcaagaa atctgtatgag acacaaacat 2852
 tggacttcaa gacagttta aattttgggt aatgaactt tatttcctgt ttatagacgt 2912
 actaataaaaa aagaagttga ttagtgcattt agtggtaaga ttgttactaa tgggttggc 2972
 aaattgtgtt aaagagccag atagtaagca ttatggcat tggcttat ctttcctgccc 3032
 acaaccatgt gacagttagt gctttgttagg actgagagca gccataaaatg acatgtaaat 3092
 gataaactgt ggctgtgctt taataaaaact ttatattacaa aaaaaaaaaaaa aaa 3145

gcggccgctc	ccggccggcc	caaggacag	agccaggctc	cgggagcccg	caacactctg	60
cctgagagcc	ccggctcctc	agcccgtac	gccaggccc	tgggctccg	cccccgactc	120
ccgagctcct	gccttagagt	cgactyggct	cccggccg	tggacagac	agacggacag	180
ccagccctgc	gagggcgcgc	ggaccggcg	gaggtgttgc	aggaggagac	cgaggagggg	240
ggctgggctg	ggctggggc	cgccggca	agagagacat	gcatggtg	accaagccga	300
gcggacggac	agcgccccc	ag	atg cag	gtg agc	agg atg	352
			Met	Gln	Val	Gly
			1	5	10	
ggt atg	aga agc	atg ccc	agc ccc	ctc ctg	gcc tgc	400
Gly Met	Arg Ser	Met Pro	Ser Pro	Leu Leu	Ala Cys	
15	20	25				
ctc ctg	ctg gta	ctg ggc	tca gtg	ctg tca	ggc tct	448
Leu Leu	Leu Val	Leu Gly	Ser Val	Leu Ser	Gly Ser	
30	35	40				
ccg ccc	cgc tgc	gag tgc	tca gcg	cag gac	cga gcc	496
Pro Pro	Arg Cys	Glu Cys	Ser Ala	Gln Asp	Arg Ala	
45	50	55				
cgc aaa	cgc ttt	gtg gcg	gtg ccc	gag ggc	atc ccc	544
Arg Lys	Arg Phe	Val Ala	Val Pro	Glu Gly	Ile Pro	
60	65	70				
ctg ctg	gac ctg	ggc aaa	aac cgc	atc aag	aca ctc	592
Leu Leu	Asp Leu	Gly Lys	Asn Arg	Ile Lys	Thr Leu	
75	80	85				
ttt gcc	agc ttc	cca cac	ctg gag	gag cta	gaa ctc	640
Phe Ala	Ser Phe	Pro His	Leu Glu	Glu Leu	Leu Asn	
95	100	105				
gtg agc	gcc gtg	gag cca	ggc gcc	ttc aac	aac ctc	688
Val Ser	Ala Val	Glu Pro	Gly Ala	Phe Asn	Asn Leu	
110	115	120				
act ctg	ggg ctg	cgc agc	aac cgc	ctg aag	ctt atc	736
Thr Leu	Gly Leu	Arg Ser	Asn Arg	Leu Lys	Leu Ile	
125	130	135				
ttc acc	ggc ctc	agc aac	ttg acc	aag ctg	gac atc	784
Phe Thr	Gly Leu	Ser Asn	Leu Thr	Lys Leu	Asp Ile	
140	145	150				
atc gtc	atc ctg	cta gac	tac atg	ttc caa	gac cta	832
Ile Val	Ile Leu	Leu Asp	Tyr Met	Phe Gln	Asp Leu	
155	160	165				
tcg ctg	gag gtc	ggc gac	aac gac	ctc gtc	tac atc	880
Ser Leu	Glu Val	Gly Asp	Asn Asp	Leu Val	Tyr Ile	
175	180	185				

FIG. 8A

ttc agc ggc ctc aac agc ctg gaa cag ctg acg ctg gag aaa tgc aat 928
 Phe Ser Gly Leu Asn Ser Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn
 190 195 200

ctg acc tcc atc ccc acg gag gcg ctc tcc cac ctg cac ggc ctc atc 976
 Leu Thr Ser Ile Pro Thr Glu Ala Leu Ser His Leu His Gly Leu Ile
 205 210 215

gtc ctg cgg cta cga cat ctc aac atc aat gcc atc agg gac tac tcc 1024
 Val Leu Arg Leu Arg His Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser
 220 225 230

ttc aag agg ctg tac cga ctt aag gtc tta gag atc tcc cac tgg ccc 1072
 Phe Lys Arg Leu Tyr Arg Leu Lys Val Leu Glu Ile Ser His Trp Pro
 235 240 245 250

tac ctg gac acc ata acc ccc cgg acg cgt ggg tcg ac 1110
 Tyr Leu Asp Thr Ile Thr Pro Arg Thr Arg Gly Ser
 255 260

FIG. 8B

000000000 - 000000000

ctcctggatg tgcgcagccg cagagcgctg ctgctgtgcc taatacccat cgctgcgcac 60
 ttgacagcca gtcggcccat ccggagcccg gtcgttggg gcagc atg gcg ggg tcg 117
 Met Ala Gly Ser 1

 ccg ctg ctc tgc ggg ccg cgg gcc ggg ggc gtc ggc att ttg gtg ctg 165
 Pro Leu Leu Cys Gly Pro Arg Ala Gly Gly Val Gly Ile Leu Val Leu
 5 10 15 20

 ctg ctc ttg ggc ctt ctg agg ctg ccc ccc acc ctg tca gcg agg ccc 213
 Leu Leu Leu Gly Leu Leu Arg Leu Pro Pro Thr Leu Ser Ala Arg Pro
 25 30 35

 gtg aag gag ccc cgc agt ctg agc gca gca tcc gcg ccc ttg gtt gag 261
 Val Lys Glu Pro Arg Ser Leu Ser Ala Ala Ser Ala Pro Leu Val Glu
 40 45 50

 acg agc act ccc ctc cgc ttg cgt cgg gcc gtg ccc cga gga gag gcg 309
 Thr Ser Thr Pro Leu Arg Leu Arg Arg Ala Val Pro Arg Gly Glu Ala
 55 60 65

 gcg ggt gcg gtg cag gag ctg gcg cgg gcg ctg gcg cac ctg ctg gag 357
 Ala Gly Ala Val Gln Glu Leu Ala Arg Ala Leu Ala His Leu Leu Glu
 70 75 80

 gcc gag aga cag gaa cgc gcg cgt gct gag gcg cag gag gct gag gat 405
 Ala Glu Arg Gln Glu Arg Ala Arg Ala Glu Ala Gln Glu Ala Glu Asp
 85 90 95 100

 cag cag gcg cgt gtc ctg gcg cag ctg ctc gac gcc tgg ggc tct ccg 453
 Gln Gln Ala Arg Val Leu Ala Gln Leu Leu Arg Ala Trp Gly Ser Pro
 105 110 115

 cgt gcc tcg gac ccg ccc ttg gcc ccc gac gat gac ccg gac gct cca 501
 Arg Ala Ser Asp Pro Pro Leu Ala Pro Asp Asp Asp Pro Asp Ala Pro
 120 125 130

 gct gca cag ctc gcc cgt gct ctg ctc cga gct cgc cta gac ccc ggc 549
 Ala Ala Gln Leu Ala Arg Ala Leu Leu Arg Ala Arg Leu Asp Pro Gly
 135 140 145

 ccc cag tgt atg atg atg gcc cca ctg gcc cag acg tcg agg atg ccg 597
 Pro Gln Cys Met Met Ala Pro Leu Ala Gln Thr Ser Arg Met Pro
 150 155 160

 gcg acg aga ctc ctg acg tgg acc ctg agc tgc tgaggtactt gctagggcgg 650
 Ala Thr Arg Leu Leu Thr Trp Thr Leu Ser Cys
 165 170 175

 atcctcaccg gaagttcgga gccagaggct gtcctgcct cgcgcgcct ccgcgcgcct 710
 gtggaccagg attgggtcc cgaggtgcct cctgagaacg tactgggggc tctgctacgc 770
 gtcaaacgcc tggagaaccc ctgcgcgcag gcgccqgcac qccqccctctt qccctccctga 830

FIG. 9A

gctgtgtgc atcctgcacg cccttggacc caggagcgcc ccagcaaccc tgactccctg 890
ccagcacgtc caaggctgct taccggcagca acctcccatc ccctgagccc tcaataaattg 950
ccatctgttag caaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa 1010
aaaaaaaaaaa aaaaaaaaaa 1027

FIG. 9B